

PCT09

RAW SEQUENCE LISTING

DATE: 08/14/2001

PATENT APPLICATION: US/09/890,806

TIME: 10:59:06

Input Set : A:\59399 seq.txt

Output Set: N:\CRF3\08142001\I890806.raw

ENTERED

3 <110> APPLICANT: Johnson et al.
 5 <120> TITLE OF INVENTION: INHIBITION OF THE MHC CLASS II ANTIGEN PRESENTATION
 6 PATHWAY AND PRESENTATION TO CD4+ CELLS
 8 <130> FILE REFERENCE: 0899-59399
 of c--> 10 <140> CURRENT APPLICATION NUMBER: US/09/890,806
 c--> 11 <141> CURRENT FILING DATE: 2001-08-01
 13 <150> PRIOR APPLICATION NUMBER: US00/02740
 14 <151> PRIOR FILING DATE: 2000-02-02
 16 <150> PRIOR APPLICATION NUMBER: 60/118,287
 17 <151> PRIOR FILING DATE: 1999-02-02
 19 <160> NUMBER OF SEQ ID NOS: 7
 21 <170> SOFTWARE: PatentIn Ver. 2.1
 23 <210> SEQ ID NO: 1
 24 <211> LENGTH: 600
 25 <212> TYPE: DNA
 26 <213> ORGANISM: Cytomegalovirus
 28 <400> SEQUENCE: 1
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 30 gataaacaat accaacaggg taatgtttat ggagtaaaac actattgtcc aggccacatg 120
 31 cgtgtatgac ttccgcacca tcccgtactg catgttccac atgtacgcgc tagacgtgta 180
 32 atccactcgc agttcgggga cgcaacgcag ccagatcaca tccccttgca gtaccagacg 240
 33 cagggctagc gtctcgaaga tcggcatcac atctaagttc cgcacgttcc actttaacga 300
 34 ctccccggga acgaactcca cgtcgtcggc gtgtacgtac aggttctctc ccacgccgcc 360
 35 ataatcggcc ttccggtcga agacgaaccg actcatgttg cccacgatgc tcccccgagc 420
 36 aaacaacttg ccgttgtcaa tgtagcaccg gttgtcctcg atttgaaacc agggatgctt 480
 37 ggccgtggac ttccagggcc ggagcgcgct tccccggct ttagtgattc catcgggcag 540
 38 gcggatcaag ggacccatgg aggtccaaag acccaccacg gctttccaga gattgttcat 600
 41 <210> SEQ ID NO: 2
 42 <211> LENGTH: 600
 43 <212> TYPE: DNA
 44 <213> ORGANISM: cytomegalovirus
 46 <220> FEATURE:
 47 <221> NAME/KEY: CDS
 48 <222> LOCATION: (1)..(600)
 50 <400> SEQUENCE: 2
 51 atg aac aat ctc tgg aaa gcc tgg gtg ggt ctt tgg acc tcc atg ggt 48
 52 Met Asn Asn Leu Trp Lys Ala Trp Val Gly Leu Trp Thr Ser Met Gly
 53 1 5 10 15
 55 ccc ttg atc cgc ctg ccc gat gga atc act aaa gcc ggg gaa gac gcg 96
 56 Pro Leu Ile Arg Leu Pro Asp Gly Ile Thr Lys Ala Gly Glu Asp Ala
 57 20 25 30
 59 ctc cgg ccc tgg aag tcc acg gcc aag cat ccc tgg ttt caa atc gag 144
 60 Leu Arg Pro Trp Lys Ser Thr Ala Lys His Pro Trp Phe Gln Ile Glu
 61 35 40 45
 63 gac aac cgg tgc tac att gac aac ggc aag ttg ttt gct cgg ggg agc 192
 64 Asp Asn Arg Cys Tyr Ile Asp Asn Gly Lys Leu Phe Ala Arg Gly Ser
 65 50 55 60

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67 atc gtg ggc aac atg agt cgg ttc gtc ttc gat ccg aag gcc gat tat 240
68 ile Val Gly Asn Met Ser Arg Phe Val Phe Asp Pro Lys Ala Asp Tyr
69 65 70 75 80
71 ggc ggc gtg gga gag aac ctg tac gta cac gcc gac gac gtg gag ttc 288
72 Gly Gly Val Gly Glu Asn Leu Tyr Val His Ala Asp Asp Val Glu Phe
73 85 90 95
75 gtt ccc ggg gag tcg tta aag tgg aac gtg cgg aac tta gat gtg atg 336
76 Val Pro Gly Glu Ser Leu Lys Trp Asn Val Arg Asn Leu Asp Val Met
77 100 105 110
79 ccg atc ttc gag acg cta gcc ctg cgt ctg gta ctg caa ggg gat gtg 384
80 Pro Ile Phe Glu Thr Leu Ala Leu Arg Leu Val Leu Gln Gly Asp Val
81 115 120 125
83 atc tgg ctg cgt tgc gtc ccc gaa ctg cga gtg gat tac acg tct agc 432
84 Ile Trp Leu Arg Cys Val Pro Glu Leu Arg Val Asp Tyr Thr Ser Ser
85 130 135 140
87 gcg tac atg tgg aac atg cag tac ggg atg gtg cgg aag tca tac acg 480
88 Ala Tyr Met Trp Asn Met Gln Tyr Gly Met Val Arg Lys Ser Tyr Thr
89 145 150 155 160
91 cat gtg gcc tgg aca ata gtg ttt tac tcc ata aac att acc ctg ttg 528
92 His Val Ala Trp Thr Ile Val Phe Tyr Ser Ile Asn Ile Thr Leu Leu
93 165 170 175
95 gta ttg ttt atc gtg tat gtg act gtg gac tgt aac ttg tct atg atg 576
96 Val Leu Phe Ile Val Tyr Val Thr Val Asp Cys Asn Leu Ser Met Met
97 180 185 190
99 tgg atg cgg ttt ttc gtg tgc tga 600
100 Trp Met Arg Phe Phe Val Cys
101 195 199
104 <210> SEQ ID NO: 3
105 <211> LENGTH: 199
106 <212> TYPE: PRT
107 <213> ORGANISM: cytomegalovirus
109 <400> SEQUENCE: 3
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111 1 5 10 15
112 Pro Leu Ile Arg Leu Pro Asp Gly Ile Thr Lys Ala Gly Glu Asp Ala
113 20 25 30
114 Leu Arg Pro Trp Lys Ser Thr Ala Lys His Pro Trp Phe Gln Ile Glu
115 35 40 45
116 Asp Asn Arg Cys Tyr Ile Asp Asn Gly Lys Leu Phe Ala Arg Gly Ser
117 50 55 60
118 Ile Val Gly Asn Met Ser Arg Phe Val Phe Asp Pro Lys Ala Asp Tyr
119 65 70 75 80
120 Gly Gly Val Gly Glu Asn Leu Tyr Val His Ala Asp Asp Val Glu Phe
121 85 90 95
122 Val Pro Gly Glu Ser Leu Lys Trp Asn Val Arg Asn Leu Asp Val Met
123 100 105 110
124 Pro Ile Phe Glu Thr Leu Ala Leu Arg Leu Val Leu Gln Gly Asp Val
125 115 120 125
126 Ile Trp Leu Arg Cys Val Pro Glu Leu Arg Val Asp Tyr Thr Ser Ser

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127      130      135      140
128 Ala Tyr Met Trp Asn Met Gln Tyr Gly Met Val Arg Lys Ser Tyr Thr
129 145      150      155      160
130 His Val Ala Trp Thr Ile Val Phe Tyr Ser Ile Asn Ile Thr Leu Leu
131      165      170      175
132 Val Leu Phe Ile Val Tyr Val Thr Val Asp Cys Asn Leu Ser Met Met
133      180      185      190
134 Trp Met Arg Phe Phe Val Cys
135      195
139 <210> SEQ ID NO: 4
140 <211> LENGTH: 534
141 <212> TYPE: DNA
142 <213> ORGANISM: Artificial Sequence ✓
144 <220> FEATURE:
145 <223> OTHER INFORMATION: Description of Artificial Sequence:chimera ✓
147 <220> FEATURE:
148 <221> NAME/KEY: CDS
149 <222> LOCATION: (1)..(534)
151 <400> SEQUENCE: 4
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153 Met Lys Phe Leu Val Asn Val Ala Leu Val Phe Met Val Val Tyr Ile
154 1 5 10 15
156 tct tac atc tat gcg cgc ctg ccc gat gga atc act aaa gcc ggg gaa 96
157 Ser Tyr Ile Tyr Ala Arg Leu Pro Asp Gly Ile Thr Lys Ala Gly Glu
158 20 25 30
160 gac gcg ctg cgg ccc tgg aag tcc acg gcc aag cat ccc tgg ttt caa 144
161 Asp Ala Leu Arg Pro Trp Lys Ser Thr Ala Lys His Pro Trp Phe Gln
162 35 40 45
164 atc gag gac aac cgg tgc tac att gac aac ggc aag ttg ttt gct cgg 192
165 Ile Glu Asp Asn Arg Cys Tyr Ile Asp Asn Gly Lys Leu Phe Ala Arg
166 50 55 60
168 ggg agc atc gtg ggc aac atg agt cgg ttc gtc ttc gat ccg aag gcc 240
169 Gly Ser Ile Val Gly Asn Met Ser Arg Phe Val Phe Asp Pro Lys Ala
170 65 70 75 80
172 gat tat ggc ggc gtg gga gag aac ctg tac gta cac gcc gac gac gtg 288
173 Asp Tyr Gly Gly Val Gly Glu Asn Leu Tyr Val His Ala Asp Asp Val
174 85 90 95
176 gag ttc gtt ccc ggg gag tgc tta aag tgg aac gtg cgg aac tta gat 336
177 Glu Phe Val Pro Gly Glu Ser Leu Lys Trp Asn Val Arg Asn Leu Asp
178 100 105 110
180 gtg atg ccg atc ttc gag acg cta gcc ctg cgt ctg gta ctg caa ggg 384
181 Val Met Pro Ile Phe Glu Thr Leu Ala Leu Arg Leu Val Leu Gln Gly
182 115 120 125
184 gat gtg atc tgg ctg cgt tgc gtc ccc gaa ctg cga gtg gat tac acg 432
185 Asp Val Ile Trp Leu Arg Cys Val Pro Glu Leu Arg Val Asp Tyr Thr
186 130 135 140
188 tct agc gcg tac atg tgg aac atg cag tac ggg atg gtg ggg cag cca 480
189 Ser Ser Ala Tyr Met Trp Asn Met Gln Tyr Gly Met Val Gly Gln Pro
190 145 150 155 160

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192 gaa ctc gcc ccg gaa gac ccc gag gat tcg gcc ctc ttg gag gac ccc 528
193 Glu Leu Ala Pro Glu Asp Pro Glu Asp Ser Ala Leu Leu Glu Asp Pro
194                               165                               170                               175
196 gtg tga 534
197 Val
200 <210> SEQ ID NO: 5
201 <211> LENGTH: 177
202 <212> TYPE: PRT
203 <213> ORGANISM: Artificial Sequence ✓
205 <220> FEATURE:
206 <223> OTHER INFORMATION: Description of Artificial Sequence:chimera ✓
208 <400> SEQUENCE: 5
209 Met Lys Phe Leu Val Asn Val Ala Leu Val Phe Met Val Val Tyr Ile
210 1 5 10 15
211 Ser Tyr Ile Tyr Ala Arg Leu Pro Asp Gly Ile Thr Lys Ala Gly Glu
212 20 25 30
213 Asp Ala Leu Arg Pro Trp Lys Ser Thr Ala Lys His Pro Trp Phe Gln
214 35 40 45
215 Ile Glu Asp Asn Arg Cys Tyr Ile Asp Asn Gly Lys Leu Phe Ala Arg
216 50 55 60
217 Gly Ser Ile Val Gly Asn Met Ser Arg Phe Val Phe Asp Pro Lys Ala
218 65 70 75 80
219 Asp Tyr Gly Gly Val Gly Glu Asn Leu Tyr Val His Ala Asp Asp Val
220 85 90 95
221 Glu Phe Val Pro Gly Glu Ser Leu Lys Trp Asn Val Arg Asn Leu Asp
222 100 105 110
223 Val Met Pro Ile Phe Glu Thr Leu Ala Leu Arg Leu Val Leu Gln Gly
224 115 120 125
225 Asp Val Ile Trp Leu Arg Cys Val Pro Glu Leu Arg Val Asp Tyr Thr
226 130 135 140
227 Ser Ser Ala Tyr Met Trp Asn Met Gln Tyr Gly Met Val Gly Gln Pro
228 145 150 155 160
229 Glu Leu Ala Pro Glu Asp Pro Glu Asp Ser Ala Leu Leu Glu Asp Pro
230 165 170 175
231 Val
235 <210> SEQ ID NO: 6
236 <211> LENGTH: 33
237 <212> TYPE: DNA ✓
238 <213> ORGANISM: Artificial Sequence
240 <220> FEATURE:
241 <223> OTHER INFORMATION: Description of Artificial Sequence:oligonucleotide ✓
243 <400> SEQUENCE: 6
244 cgcggatcca tgaacaatct ctggaaagcc tgg 33
247 <210> SEQ ID NO: 7
248 <211> LENGTH: 33
249 <212> TYPE: DNA
250 <213> ORGANISM: Artificial Sequence ✓
252 <220> FEATURE:
253 <223> OTHER INFORMATION: Description of Artificial Sequence:oligonucleotide ✓

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255 <400> SEQUENCE: 7

256 cgtgaattcg acatgacaca cgtaatgggt act

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VERIFICATION SUMMARY

DATE: 08/14/2001

PATENT APPLICATION: US/09/890,806

TIME: 10:59:07

Input Set : A:\59399 seq.txt

Output Set: N:\CRF3\08142001\I890806.raw

L:10 M:270 C: Current Application Number differs, Replaced Application Number

L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date